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# SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT:

Bazin, Hervé

Latinne, Dominique

Kaplan, Ruth

Kieber-Emmons, Thomas

Postema, Christina E.

White-Scharf, Mary

(ii) TITLE OF INVENTION: LO-CD2a Antibody and Uses

Thereof for Inhibiting

T-Cell Activation and

Proliferation

- (iii) NUMBER OF SEQUENCES: 96
- (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE

Carella, Byrne, Bain, Gilfillan,

Cecchi, Stavart & Olstein

- (B) STREET: 6 Becker Farm Road
- (C) CITY: Roseland
- (D) STATE: New Jersey
- (E) COUNTRY: U.S.A.
- (F) ZIP: 0706\$
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5 inch diskette
  - (B) COMPUTER: IBM PS/2
  - (C) OPERATING SYSTEM: MS-DOS

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- (D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/477,989
  - (B) FILING DATE: 07-JUN-1995
  - (C) CLASSIFICATION:

#### (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/407,009
- (B) FILING DATE: 29-MAR-1995
- (A) APPLICATION NUMBER: 08/119,032
- (B) FILING DATE: 09-SEP-1993
- (A) APPLICATION NUMBER: 08/027,008
- (B) FILING DATE: 05-MAR-1993

# (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Olstein, Elliot M.
- (B) REGISTRATION NUMBER: 24,025
- (C) REFERENCE/DOCKET NUMBER: 61750-147

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744

- (2) INFORMATION FOR SEQ ID NO: 1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 32 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: oligonucleotide
  - (ix) FEATURE:
    - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AACCCGGGGA CATTCAGCTG ACCCAGTCTC AA

32

- (2) INFORMATION FOR SEQ ID NO: 2:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CAGTCGACTA CAGTTGGTGC AGCATCAGC

- (2) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

  AACCCGGGGA GGTCCAGCTG CAGCAGTCTG G
  - (2) INFORMATION FOR SEQ ID NO: 4:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: oligonucleotide
  - (ix) FEATURE:
    - (A) NAME/KEY: PCR primer
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAGTCGACCC AGTGGATAGA CCGATGG

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	(2)	INFORMATION FOR SEQ ID NO: 5:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 22 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
CCGCAAGCTT CA	ATGGGA'	TGG AG	22
	(2)	INFORMATION FOR SEQ ID NO: 6:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 27 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEOUENCE DESCRIPTION: SEQ ID NO: 6:	

27

GCTGCTTGGG GACTGGGTCA GCTGGAT

(2) INFORMATION FOR SEQ ID NO: 7:

U

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
  ATTCAGCTGA CCCAGTCTCC A
  - (2) INFORMATION FOR SEQ ID NO: 8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 58 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: oligonucleotide
  - (ix) FEATURE:
    - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

  GATCGGATCC ACCTGAGGAA GCAAAGTTTA AATTCTACTC ACGTTTCAGT TCCAGCTT

- (2) INFORMATION FOR SEQ ID NO: 9:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
  - (2) INFORMATION FOR SEQ ID NO: 10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 bases
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: oligonucleotide
  - (ix) FEATURE:
    - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGGTCCAGC TGCAGCAGTC T

21

- (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGATGTATCA GCTGTCAGTG TGGC

24

- (2) INFORMATION FOR SEQ ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCCACACTGA CAGCTGATAC ATCG

- (2) INFORMATION FOR SEQ ID NO: 13:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

### CAGAGTGCCT TGGCCCCAGT A

21

- (2) INFORMATION FOR SEQ ID NO: 14:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TACTGGGGCC AAGGCACCCT CGTCACA

- (2) INFORMATION FOR SEQ ID NO: 15:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCGGATCC CTATAAATCT CTGGC

25

- (2) INFORMATION FOR SEQ ID NO: 16:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGGATCCGC GGCCGCGTCG ACTACAGTTG GTGCAGCATC AGC

- (2) INFORMATION FOR SEQ ID NO: 17:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide

#### (ix) FEATURE:

- (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGGATCCGC GGCCGCGTCG ACCCAGTGGA TAGACCGATG G

41

- (2) INFORMATION FOR SEQ ID NO: 18:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CCATGGCCTC GAGGGCCCCC CCCCCCCCC C

- (2) INFORMATION FOR SEQ ID NO: 19:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CCTGTTTAGG CCTCTGCTTC ACCCAGTAC

29

- (2) INFORMATION FOR SEQ ID NO: 20:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGATAATGGG TAAATTGCAT GCAGTAATA

- (2) INFORMATION FOR SEQ ID NO: 21:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

### TGCAAGCTTC ATGATGAGTC CTGTCCAGTC

30

- (2) INFORMATION FOR SEQ ID NO: 22:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AGTAAGCTTC ATGAAATGCA GGTGGATC

	(i)	EQUENCE CHARACTERISTICS:								
		(A) LENGTH: 24 bases								
		(B) TYPE: nucleic acid								
		(C) STRANDEDNESS: single								
		(D) TOPOLOGY: linear								
	(ii)	MOLECULE TYPE: oligonucleotide								
	(ix)	FEATURE:								
		(A) NAME/KEY: PCR primer								
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 23:								
GGGAGATTGC TO	CAGCT	GGA CTTC	24							
	(2)	INFORMATION FOR SEQ ID NO: 24:								
	(i)	SEQUENCE CHARACTERISTICS:								
		(A) LENGTH: 33 bases								
		(B) TYPE: nucleic acid								
		(C) STRANDEDNESS: single								
		(D) TOPOLOGY: linear								
	(ii)	MOLECULE TYPE: oligonucleotide								
	(ix)	FEATURE:								
		(A) NAME/KEY: PCR primer								
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 24:								
GATCCCCGGG CC	CACCAT	GAT GAGTCCTGTC CAG	33							
	(2)	INFORMATION FOR SEQ ID NO: 25:								

INFORMATION FOR SEQ ID NO: 23:

(2)

	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 25:	
AGAATGGCCA CGTCAT	CCGA CCCCTCAGA GTTTACTATT CTACTATCCA ACTGAGGAAG	60
C		61
(-)		
(2)	INFORMATION FOR SEQ ID NO: 26:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 34 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 26:	
GATCGAATTC GCCACCA	ATGA AATGCAGGTG GATC	34

SEQUENCE CHARACTERISTICS:

LENGTH: 61 bases

(B) TYPE: nucleic acid

(i)

(A)

INFORMATION FOR SEQ ID NO: 27: (2) SEQUENCE CHARACTERISTICS: (i) (A) LENGTH: 37 bases TYPE: nucleic acid (B) (C) STRANDEDNESS: single TOPOLOGY: linear (D) (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27: CCAGAAAGCT AGCTTGCCAT CCCTATAAAT CTCTGGC INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: (i) LENGTH: 23 amino acids (A) TYPE: amino acid (B) (C) STRANDEDNESS: TOPOLOGY: linear (D)

37

- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Val Val Leu Thr Gln Thr Pro Pro Thr

5

10

Leu Leu Ala Thr Ile Gly Gln Ser Val Ser

20 15

Ile Ser Cys

(2)

- (2) INFORMATION FOR SEQ ID NO: 29:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Asp Val Val Met Thr Gln Ser Pro Leu Ser

5

10

Leu Pro Val Thr Leu Gly Gln Pro Ala Ser

15 20

Ile Ser Cys

- (2) INFORMATION FOR SEQ ID NO: 30:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Trp Leu Leu Gln Arg Thr Gly Gln Ser Pro

5

10

Gln Pro Leu Ile Tyr

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31
Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro
5 10
Arg Arg Leu Ile Tyr
15
(2) INFORMATION FOR SEQ ID NO: 32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32
Gly Val Pro Asn Arg Phe Ser Gly Ser Gly
5 10

INFORMATION FOR SEQ ID NO: 31:

(2)

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser 15 Gly Val Glu Ala Glu Asp Leu Gly Val Tyr 25

Tyr Cys

- INFORMATION FOR SEO ID NO: 33: (2)
  - SEQUENCE CHARACTERISTICS: (i)
    - (A) LENGTH: 32 amino acids

20

30

10

- TYPE: amino acid (B)
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

5

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser

15 20

Arg Val Glu Ala Glu Asp Val Gly Val Tyr

30 25

Tyr Cys

- INFORMATION FOR SEQ ID NO: 34: (2)
  - SEQUENCE CHARACTERISTICS: (i)
    - LENGTH: 10 amino acids (A)

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys

5

10

- (2) INFORMATION FOR SEQ ID NO: 35:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 10 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO: 36:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 81 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

	(ii)	MOLECULE TYPE: oligonucleotide					
	(ix)	FEATURE:					
		(A) NAME/KEY: PCR primer					
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 36:					
GCAAGAGATG GAAGCTGGTT GTCCCAAGGT TACCAATAAT GAAGGTGGAC TCTGGGTCAT							
CACAACATCA C	CATTGG	TTTC C	81				
(2)	INFO	RMATION FOR SEQ ID NO: 37:					
	(i)	SEQUENCE CHARACTERISTICS:					
		(A) LENGTH: 72 bases					
		(B) TYPE: nucleic acid					
		(C) STRANDEDNESS: single					
		(D) TOPOLOGY: linear					
	(ii)	MOLECULE TYPE: oligonucleotide					
	(ix)	FEATURE:					
		(A) NAME/KEY: PCR primer					
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 37:					
CAACCAGCTT C	CATCTC'	TTG CAGGTCAAGT CAGAGTCTCT TACATAGTAG TGGAAACACC	60				
TATTTAATT GG			72				
(2)	INFOR	RMATION FOR SEQ ID NO: 38:					
	(i)	SEQUENCE CHARACTERISTICS:					
		(A) LENGTH: 81 bases					
		(B) TYPE: nucleic acid					
		(C) STRANDEDNESS: single					

(D)

TOPOLOGY:

linear

	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 38:	
AGATTCCAGT T	TGGATA	CCA AATAAATTAG CGGCTGTGGA GATTGGCCTG GCCTTAGCAA	60
CCAATTTAAA T	'AGGTGT	TTC C	81
(2)	INFO	RMATION FOR SEQ ID NO: 39:	
	(i)	SEQUENCE CHARACTERISTICS:	
·		(A) LENGTH: 81 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 39:	
TTGGTATCCA A	ACTGGA	ATC TGGGGTCCCC GACAGGTTCA GTGGCTCAGG GAGTGGAACA	60
GATTTCACAC T	'CAAAAT	CAG T	81
(2)	INFO	RMATION FOR SEQ ID NO: 40:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 72 bases	
		(B) TYPE: nucleic acid	
	•	(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
ATGGGTAAAT T	GCATGC	AGT AATAAACCCC CACATCCTCA GCTTCCACTC CACTGATTTT	60
GAGTGTGAAA T	'C		72
(-)			
(2)	INFO	RMATION FOR SEQ ID NO: 41:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 63 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 41:	
TACTGCATGC A	ATTTAC	CCA TTATCCGTAC ACGTTTGGAC AAGGGACCAA GCTGGAAATC	60
AAA			63
(2)	INFO	RMATION FOR SEQ ID NO: 42:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 67 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	

linear

(D) TOPOLOGY:

	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 42:	
GATCGGATCC	AACTGAG	GAA GCAAAGTTTA AATTCTACTC ACGTTTGATT TCCAGCTTGG	60
TCCCTTG			67
(2)	INFO	RMATION FOR SEQ ID NO: 43:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 23 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 43:	
GATCAAGCTT (	CATGATG	AGT CCT	23
(2)	INFO	RMATION FOR SEQ ID NO: 44:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: oligonucleotide

	(1X)	FEATURE:									
		(A) NAME/KEY: PCR primer									
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 44:									
GCAAGAGATG G	AAGCTC	GGTT G	21								
(2)	INFO	RMATION FOR SEQ ID NO: 45:									
	(i)	SEQUENCE CHARACTERISTICS:									
		(A) LENGTH: 21 bases									
		(B) TYPE: nucleic acid									
		(C) STRANDEDNESS: single									
		(D) TOPOLOGY: linear									
	(ii)	MOLECULE TYPE: oligonucleotide									
	(ix) FEATURE:										
		(A) NAME/KEY: PCR primer									
	(xi)	SEQUENCE DESCRIPTION: SÈQ ID NO: 45:									
CAACCAGCTT C	CATCTC	TTG C	21								
(2)	INFO	RMATION FOR SEQ ID NO: 46:									
	(i)	SEQUENCE CHARACTERISTICS:									
		(A) LENGTH: 21 bases									
		(B) TYPE: nucleic acid									
		(C) STRANDEDNESS: single									
		(D) TOPOLOGY: linear									
	(ii)	MOLECULE TYPE: oligonucleotide									
	(ix)	FEATURE:									

PCR primer

(A)

NAME/KEY:

	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 46:	
AGATTCCAGT	PTGGATA	CCA A	21
(2)	INFO	RMATION FOR SEQ ID NO: 47:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 47:	
TTGGTATCCA A	AACTGGA	ATC TGGG	24
(2)	INFO	RMATION FOR SEQ ID NO: 48:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
ATGGGTAAAT	rgcatgo	AGT AATA	24

(2)	INFO	RMATION FOR SEQ ID NO: 49:									
	(i)	SEQUENCE CHARACTERISTICS:									
		(A) LENGTH: 24 bases									
		(B) TYPE: nucleic acid									
		(C) STRANDEDNESS: single									
		(D) TOPOLOGY: linear									
	(ii)	MOLECULE TYPE: oligonucleotide									
	(ix)	FEATURE:									
		(A) NAME/KEY: PCR primer									
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 49:									
TACTGCATGC A	ATTTAC	CCA TTAT	24								
(2)	INFO	RMATION FOR SEQ ID NO: 50:									
	(i)	SEQUENCE CHARACTERISTICS:									
		(A) LENGTH: 26 bases									
		(B) TYPE: nucleic acid									
		(C) STRANDEDNESS: single									
		(D) TOPOLOGY: linear									
	(ii)	MOLECULE TYPE: oligonucleotide									
	(ix)	FEATURE:									
		(A) NAME/KEY: PCR primer									
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 50:									
GATCGGATCC A	ACTGAG	GAA GCAAAG	26								
(2)	INFO	RMATION FOR SEQ ID NO: 51:									
	(i)	SEQUENCE CHARACTERISTICS:									

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu

5

10

Leu Gln Arg Pro Gly Ala Ser Val Lys Leu

15

20

10

Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr

25 30

- (2) INFORMATION FOR SEQ ID NO: 52:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu

Val Lys Lys Pro Gly Ala Ser Val Lys Val

5

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
25

- (2) INFORMATION FOR SEQ ID NO: 53:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Trp Val Lys Gln Arg Pro Lys Gln Gly Leu

5

10

Glu Leu Val Gly

- (2) INFORMATION FOR SEQ ID NO: 54:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

## Glu Trp Met Gly

(2)		INF	ORMATIO	ON FO	OR SI	EQ II	OM C	: 55:			
		(i)	SEQUI	ENCE	CHAI	RACTI	ERIS	rics:			
			(A)	LENG	STH:	32 a	amino	o acid	ls		
			(B)	TYPE	E: a	amino	o ac	id			
			(C)	STRA	ANDEI	ONES	S:				
			(D)	TOPO	OLOGY	Z: ]	linea	ar			
		(ii)	) MOLE	CULE	TYPE	2: p	olyr	peptio	le		
		(xi)	) SEQUE	ENCE	DESC	CRIPT	rion:	: SEÇ	] ID	NO:	55:
Lys	Ala	Thr Le	eu Thr	Ala	Asp	Thr	Ser	Ser			
			5					10			
Asn	Thr	Ala Ty	yr Met	Gln	Leu	Ser	Ser	Leu			
			15					20			
Thr	Ser	Glu As	sp Thr	Ala	Thr	Tyr	Phe	Cys			

Ala Arg

(2) INFORMATION FOR SEQ ID NO: 56:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56: Arg Val Thr Met Thr Arg Asp Thr Ser Ile 5 10 Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu 15 20 Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys 30 25

Ala Arg

- INFORMATION FOR SEQ ID NO: 57: (2)
  - (i) SEQUENCE CHARACTERISTICS:
    - LENGTH: 11 amino acids (A)
    - (B) TYPE: amino acid
    - STRANDEDNESS: (C)
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Trp Gly Gln Gly Thr Leu Val Thr Val Ser

5

10

Ser

- INFORMATION FOR SEQ ID NO: 58: (2)
  - (i) SEQUENCE CHARACTERISTICS:
    - LENGTH: 11 amino acids (A)
    - TYPE: amino acid (B)

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
Trp Gly Gln Gly Thr Leu Val Thr Val Ser
5 10
Ser
(2) INFORMATION FOR SEQ ID NO: 59:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: oligonucleotide
(ix) FEATURE:
(A) NAME/KEY: PCR primer
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:
GATCAAGCTT CATGAAATGC AGGTGGATCA TCCTCTTCTT GATGGCAGTA GCTACAGGTA 60
AGGCACTCCC AAGTCGTAAA CTTGAGA 88
(2) INFORMATION FOR SEQ ID NO: 60:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS, single

(C)

STRANDEDNESS:

		(D) TOPOLOGY: linear			
	(ii)	MOLECULE TYPE: oligonucleotide			
	(ix)	FEATURE:			
		(A) NAME/KEY: PCR primer			
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 60:			
CACCTGTGAG I	TGACCC	CCTG TTGAAAGAAA TCCAAAGATA GTGTCACTGT CTCCCAAGTG	60		
TATGATCTCT C	TATGATCTCT CAAGTTTAGG ACTTGGG				
(2)	INFO	RMATION FOR SEQ ID NO: 61:			
	(i)	SEQUENCE CHARACTERISTICS:			
		(A) LENGTH: 78 bases			
		(B) TYPE: nucleic acid			
		(C) STRANDEDNESS: single			
		(D) TOPOLOGY: linear			
	(ii)	MOLECULE TYPE: oligonucleotide			
	(ix)	FEATURE:			
		(A) NAME/KEY: PCR primer			
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 61:			
ACAGGGGTCA A	.CTCACA	AGGT GCAGCTGGTG CAGTCTGGGG CTGAGGTGAA GAAGCCTGGG	60		
GCCTCAGTGA A	GGTCTC	cc	78		
(2)	INFO	RMATION FOR SEQ ID NO: 62:			
	(i)	SEQUENCE CHARACTERISTICS:			
		(A) LENGTH: 78 bases			
		(B) TYPE: nucleic acid			
		(C) CTDANDEDNESS, gingle			

(D) TOPO	OLOGY: linear
(ii) MOLECULE	TYPE: oligonucleotide
(ix) FEATURE:	
(A) NAMI	E/KEY: PCR primer
(xi) SEQUENCE	DESCRIPTION: SEQ ID NO: 62:
GGCCTGTCGC ACCCAGTACA TATAGTA	CTC GGTGAAGGTG TATCCAGAAG CCTTGCAGGA 60
GACCTTCACT GAGGCCCC	78
(2) INFORMATION FO	OR SEQ ID NO: 63:
(i) SEQUENCE	CHARACTERISTICS:
(A) LENC	GTH: 78 bases
(B) TYPE	E: nucleic acid
(C) STR	ANDEDNESS: single
(D) TOPO	OLOGY: linear
(ii) MOLECULE	TYPE: oligonucleotide
(ix) FEATURE:	
(A) NAME	E/KEY: PCR primer
(xi) SEQUENCE	DESCRIPTION: SEQ ID NO: 63:
ATGTACTGGG TGCGACAGGC CCCTGGAC	CAA GGGCTTGAGC TGATGGGAAG GATCGATCCT 60
GAAGACGGTA GTATTGAT	78
(2) INFORMATION FO	OR SEQ ID NO: 64:
(i) SEQUENCE	CHARACTERISTICS:
(A) LENC	GTH: 78 bases
(B) TYPE	E: nucleic acid
(C) STRA	ANDEDNESS: single

(ii) MOI	ECULE TYPE: oligonucleotide		
(ix) FEA	ATURE:		
(A)	NAME/KEY: PCR primer		
(xi) SEQ	QUENCE DESCRIPTION: SEQ ID NO: 64:		
TGTGCTAGAG GACGTGTCAG CGGTCAGGGT GACCTTTTTC TTAAACTTCT CAACATAATC			
AATACTACCG TCTTCAGG	78		
(2) INFORMAT	CION FOR SEQ ID NO: 65:		
(i) SEQ	QUENCE CHARACTERISTICS:		
(A)	LENGTH: 84 bases		
(B)	TYPE: nucleic acid		
(C)	STRANDEDNESS: single		
(D)	TOPOLOGY: linear		
(ii) MOI	ECULE TYPE: oligonucleotide		
(ix) FEA	TURE:		
(A)	NAME/KEY: PCR primer		
(xi) SEÇ	UENCE DESCRIPTION: SEQ ID NO: 65:		
GCTGACACGT CCTCTAGCAC	AGCCTACATG GAGCTGAGCA GCCTGACCTC TGACGACACG 60		
GCCGTGTATT ACTGTGCGAG	AGGA 84		
(2) INFORMAT	TION FOR SEQ ID NO: 66:		
(i) SEQ	UENCE CHARACTERISTICS:		
(A)	LENGTH: 87 bases		
(B)	TYPE: nucleic acid		
(C)	STRANDEDNESS: single		

(D)

TOPOLOGY:

linear

(ii	MOLECULE TYPE: oligonucleotide	
(ix	) FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi	SEQUENCE DESCRIPTION: SEQ ID NO: 66:	
GGACTCACCT GAGGAC	ACGG TGACCAGGGT TCCTTGGCCC CAGTAAGCAA ACCTATAGTT	60
AAACTTTCCT CTCGCA	CAGT AATACAC	87
4-1		
(2) INFO	ORMATION FOR SEQ ID NO: 67:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 69 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 67:	
ACCGTCTCCT CAGGTG	AGTC CTTACAACCT CTCTCTTCTA TTCAGCTTAA ATAGATTTTA	60
CTGCATTTG		69
(2) INFO	DRMATION FOR SEQ ID NO: 68:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 69 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	

(D)

TOPOLOGY:

linear

	(D)	TOPOLOGY:	linear	
(ii)	MOLE	CULE TYPE:	oligonucleotide	
(ix)	FEAT	URE:		
	(A)	NAME/KEY:	PCR primer	
(xi)	SEQU	ENCE DESCRI	PTION: SEQ ID NO: 68:	
CCTAGTCCTT CATGAC	CTGA AA	ATTCAGATA CACAC	CATTTC CCCCCCAACA AATGCAGTAA	60
AATCTATTT				69
(2) INFO	RMATI	ON FOR SEQ	ID NO: 69:	
(i)	SEQU	ENCE CHARAC	TERISTICS:	
	(A)	LENGTH: 72	bases	
	(B)	TYPE: nuc	leic acid	
	(C)	STRANDEDNE	SS: single	
	(D)	TOPOLOGY:	linear	
(ii)	MOLE	CULE TYPE:	oligonucleotide	
(ix)	FEAT	URE:		
	(A)	NAME/KEY:	PCR primer	
(xi)	SEQU	ENCE DESCRI	PTION: SEQ ID NO: 69:	
TTCAGGTCAT GAAGGA	CTAG GG	ACACCTTG GGAGT	CAGAA AGGGTCATTG GGAGCCCGGG	60
CTGATGCAGA CA				72
(2) INFO	RMATI	ON FOR SEQ	ID NO: 70:	
(i)	SEQU	ENCE CHARAC	TERISTICS:	
	(A)	LENGTH: 72	bases	
	(B)	TYPE: nuc	leic acid	
	(C)	STRANDEDNE	SS: single	

		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 70:	
GATCGGATCC C	TATAAA	ATCT CTGGCCATGA AGTCTGGGAG CTGAGGATGT CTGTCTGCAT	60
CAGCCCGGGC T	С		72
(2)	INFO	RMATION FOR SEQ ID NO: 71:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 25 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 71:	
GATCAAGCTT C	ATGAAA	ATGC AGGTG	25
(2)	INFO	RMATION FOR SEQ ID NO: 72:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 23 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

		(ii)	MOLECULE TYPE: oligonucleotide	
		(ix)	FEATURE:	
			(A) NAME/KEY: PCR primer	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 72:	
	CACCTGTGAG	TGACCO	CCTG TTG	23
	(2)	INFO	RMATION FOR SEQ ID NO: 73:	
		(i)	SEQUENCE CHARACTERISTICS:	
			(A) LENGTH: 21 bases	
,			(B) TYPE: nucleic acid	
/			(C) STRANDEDNESS: single	
			(D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: oligonucleotide	
		(ix)	FEATURE:	
			(A) NAME/KEY: PCR primer	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 73:	
	ACAGGGGTCA A	ACTCACA	GGT G	21
	(2)	INFO	RMATION FOR SEQ ID NO: 74:	
		(i)	SEQUENCE CHARACTERISTICS:	
			(A) LENGTH: 21 bases	
			(B) TYPE: nucleic acid	
			(C) STRANDEDNESS: single	
			(D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: oligonucleotide	
		(ix)	FEATURE:	

		(A) NAME/KEY: PCR primer	
	(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO: 74:	
GGCCTGTCGC 1	ACCCAG	STACA T	21
(2)	INFO	ORMATION FOR SEQ ID NO: 75:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 75:	
ATGTACTGGG T	GCGACA	PAGGC C	21
(2)	INFO	ORMATION FOR SEQ ID NO: 76:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 76:	

TGTGCTAGAG GACGTGTCAG C 21

(2)	INFO	RMATION FOR SEQ ID NO: //:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 77:	
GCTGACACGT C	CTCTAC	CAC A	21
(2)	INFO	RMATION FOR SEQ ID NO: 78:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 78:	
GGACTCACCT G	AGGAGA	ACGG T	21

(2)	INFO	RMATION FOR SEQ ID NO: 79:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 79:	
ACCGTCTCCT C	AGGTGA	GTC C	21
(2)	INFO	RMATION FOR SEQ ID NO: 80:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 80:	
CCTAGTCCTT C	ATGACC	TGA A	21
(2)	INFO	RMATION FOR SEQ ID NO: 81:	
	(i)	SEQUENCE CHARACTERISTICS:	

			(A) LENGTH: 21 bases	
			(B) TYPE: nucleic acid	
			(C) STRANDEDNESS: single	
			(D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: oligonucleotide	
		(ix)	FEATURE:	
			(A) NAME/KEY: PCR primer	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 81:	
	TTCAGGTCAT (	GAACGAC	TAG G	21
	(2)	INFO	RMATION FOR SEQ ID NO: 82:	
		(i)	SEQUENCE CHARACTERISTICS:	
1			(A) LENGTH: 26 bases	
,			(B) TYPE: nucleic acid	
			(C) STRANDEDNESS: single	
			(D) TOPOLOGY: linear	
		(ii)	MOLECULE TYPE: oligonucleotide	
		(ix)	FEATURE:	
			(A) NAME/KEY: PCR primer	
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 82:	
	GATCGGATCC (	CTATAAA	TCT CTGGCC	26
	(2)	INFO	RMATION FOR SEQ ID NO: 83:	
		(i)	SEQUENCE CHARACTERISTICS:	
			(A) LENGTH: 761 bases	

(B) TYPE: nucleic acid

(C)	STRANDEDNESS:	single
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

# (ix) FEATURE:

(A) NAME/KEY: Nucleotide sequence encoding LO-CD2a  $\ensuremath{V_{\scriptscriptstyle L}}$  chain.

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

ATGATGAGTC	CTGTCCAGTC	CCTGTTTCTG	TTATTGCTTT	GGATTCTGGG	TAAGTAGAGA	60
ATGAGTTACA	GGACAAGAAT	GGGGATGGAG	GATGAGTTCT	GACTGCCCAT	GTTGGCTGTC	120
CATGTGTGGT	AAGGCAGGTC	CTATTTTCTA	AGATGGACAC	TTGAGATTCC	ATTACTTGAT	180
AATGAGAAAT	TACAGATGAG	ATAGGATTTG	TGCTAAGAGG	ATTCTAATGT	AGATGAGAAG	240
GTGTATGCCA	TTTAGGATCT	GCAACCGAAT	TGTTTTGTGA	AAAAGCATTT	GGTATATTTT	300
ТТАААААТСА	CAAAACACAC	CGGGATCTCA	CAGGAAATGA	GTAACAAAAA	GTAATTCACA	360
AAGATTGGTT	GCAAATTTTG	CACATAACTT	TGTTCTGATC	TATTATAATT	TCAGGAACCA	420
ATGGTGATGT	TGTGCTGACC	CAGACTCCAC	CTACTTTATT	GGCTACCATT	GGACAATCAG	480
TCTCCATCTC	TTGCAGGTCA	AGTCAGAGTC	TCTTACATAG	TAGTGGAAAC	ACCTATTTAA	540
ATTGGTTGCT	ACAGAGGACA	GGCCAATCTC	CACAGCCGCT	AATTTATTTG	GTATCCAAAC	600
TGGAATCTGG	GGTCCCCAAC	AGGTTCAGTG	GCAGTGGGTC	AGGAACAGAT	TTCACACTCA	660
AAATCAGTGG	AGTGGAAGCT	GAGGATTTGG	GGGTTTATTA	CTGCATGCAA	TTTACCCATT	720
ΔΤΟΟΘΤΆΘΑΟ	СТТТССАССТ	GGGACCAAGC	TGGAACTGAA	A		761

# (2) INFORMATION FOR SEQ ID NO: 84:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide



## (ix) FEATURE:

(A) NAME/KEY: Chimeric LO-CD2a V<sub>L</sub> Chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Met Met Ser Pro Val Gln Ser Leu Phe

-20 **-15** 

Leu Leu Leu Trp Ile Leu Gly Thr Asn

-10 -5

Gly Asp Val Val Leu Thr Gln Thr Pro

-1 +1 5

Pro Thr Leu Leu Ala Thr Ile Gly Gln Ser

10 15

Val Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu

20 25

Leu His Ser Ser Gly Asn Thr Tyr Leu Asn Trp

30 35 40

Leu Leu Gln Arg Thr Gly Gln Ser Pro Gln

45 50

Pro Leu Ile Tyr Leu Val Ser Lys Leu Glu

55 60

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser

65 70

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

75 80

Ser Gly Val Glu Ala Glu Asp Leu Gly Val

85 90

Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu

105 110

Leu Lys

# (2) INFORMATION FOR SEQ ID NO: 85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide

## (ix) FEATURE:

(A) NAME/KEY: Nucleotide sequence encoding LO-CD2a  $\ensuremath{V_{\scriptscriptstyle H}}$  chain.

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

ATGAAATGCA GGTGG	ATCAT CCTCTTCTTG	ATGGCAGTAG	CTACAGGTAA	GGCACTCCCA	60
AGTCCTAAAC TTGAG	AGATC ATACACTTGG	GAGACAGTGA	CACTATCTTT	GGATTTCTTT	120
CAACAGGGGT CAACT	CAGAA GTCCAGCTGC	AGCAATCTGG	GCCTGAGCTT	CAGAGACCCG	180
GGGCCTCAGT CAAGT	TGTCG TGCAAGGCTT	CTGGCTATAT	ATTTACAGAA	TACTATATGT	240
ACTGGGTGAA GCAGA	GGCCT AAACAGGGCC	TGGAATTAGT	AGGAAGGATC	GATCCTGAAG	300
ACGGTAGTAT TGATT	ATGTT GAGAAGTTCA	AAAAGAAGGC	CACACTGACT	GCAGATACAT	360
CGTCCAACAC AGCCT	ACATG CAACTCAGCA	GCCTGACATC	TGAGGACACA	GCAACCTATT	420
TTTGTGCTAG GGGAA	AATTC AACTATCGAT	TTGCTTACTG	GGGCCAAGGC	ACCCTCGTCA	480
CAGTCTCCTC A					491

(2) INFORMATION FOR SEQ ID NO: 86:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(ix) FEATURE:
(A) NAME/KEY: Amino acid sequence of chimeric LO-
CD2a $V_{\text{H}}$ chain.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:
Met Lys Cys Arg Trp Ile Ile Leu Phe Leu
-19 -15 -10
Met Ala Val Ala Thr Gly Val Asn Ser Glu
-5 -1 +1
Val Gln Leu Gln Gln Ser Gly Pro Glu
5 10
Leu Gln Arg Pro Gly Ala Ser Val Lys Leu
15 20
Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr
25 30
Glu Tyr Tyr Met Tyr Trp Val Lys Gln Arg

-47-

Pro Lys Gln Gly Leu Glu Leu Val Gly Arg

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr

55 6

Val Glu Lys Phe Lys Lys Lys Ala Thr Leu

65 70

Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr

75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp

85 90

Thr Ala Thr Tyr Phe Cys Ala Arg Gly Lys

95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln

105 110

Gly Thr Leu Val Thr Val Ser Ser

115

# (2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (ix) FEATURE:
  - (A) NAME/KEY: Rat LO-CD2a light chain variable region.

(2	(i)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	87:

Asp Val Val Leu Thr Gln Thr Pro Pro Thr

5

10

Leu Leu Ala Thr Ile Gly Gln Ser Val Ser

15 20

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu

25 30

His Ser Ser Gly Asn Thr Tyr Leu Asn Trp

35 40

Leu Leu Gln Arg Thr Gly Gln Ser Pro Gln

45 50

Pro Leu Ile Tyr Leu Val Ser Lys Leu Glu

55 60

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser

65 70

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

75 . 80

Ser Gly Val Glu Ala Glu Asp Leu Gly Val

85 90

Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu

105 110

Leu Lys

(2)		I	NFOR	ITAM	ON F	OR S	EQ I	D NO	: 88:			
		(i) SEQUENCE CHARACTERISTICS:										
		(A) LENGTH: 112 amino acids										
		(B) TYPE: amino acid										
				(C)	STR	ANDE	ONES	S:				
				(D)	TOP	OLOG	Y: :	linea	ar			
		(:	ii) 1	MOLE	CULE	TYPI	E: 1	poly	peptide	<b>:</b>		
		(:	ix)	FEAT	JRE:							
				(A)	NAMI	E/KE	Y:	Hur	manized	l LO-CD	2a	light
			,	varia	able	reg	ion.					
		(:	xi) a	SEQUI	ENCE	DESC	CRIP	rion:	: SEQ	ID NO:	88:	
Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Pro	Ser			
				5					10			
Leu	Leu	Val	Thr	Leu	Gly	Gln	Pro	Ala	Ser			
				15					20			
Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu			
				25					30			
His	Ser	Ser	Gly	Asn	Thr	Tyr	Leu	Asn	Trp			
				35					40			
Leu	Leu	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Gln			
				45					50			
Pro	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Glu			
				55					60			

chain

70

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser

65

 Gly
 Ser
 Gly
 Thr
 Asp
 Phe
 Thr
 Leu
 Lys
 Ile

 Ser
 Gly
 Val
 Glu
 Ala
 Glu
 Asp
 Val
 Gly
 Val

 Tyr
 Tyr
 Cys
 Met
 Gln
 Phe
 Thr
 His
 Tyr
 Pro

 Tyr
 Thr
 Phe
 Gly
 Gln
 Gly
 Thr
 Lys
 Leu
 Glu

 Tyr
 Thr
 Phe
 Gly
 Gln
 Gly
 Thr
 Lys
 Leu
 Glu

Bl

Ile Lys

- (2) INFORMATION FOR SEQ ID NO: 89:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Light chain vairable region of HUM5400
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Asp Val Val Met Thr Gln Ser Pro Leu Ser

5

10

Leu Pro Val Thr Leu Gly Gln Pro Ala Ser

15 20

va.	Leu	Ser	GIn	Ser	Ser	Arg	Cys	Ser	Ile
30					25				
Trp	Asn	Leu	His	Thr	Asn	Gly	Asp	Ser	Tyr
40					35				
Arg	Pro	Ser	Gln	Gly	Pro	Arg	Gln	Gln	Phe
50					45				
Asp	Arg	Asn	Ser	Val	Lys	Tyr	Ile	Leu	Arg
60					55				
Ser	Gly	Ser	Phe	Arg	Asp	Pro	Val	Gly	Ser
70					65				
Ile	Lys	Leu	Thr	Phe	Asp	Thr	Gly	Ser	Gly
80					75				
Val	Gly	Val	Asp	Glu	Ala	Glu	Val	Arg	Ser
90					85				
Pro	Trp	His	Thr	Gly	Gln	Met	Cys	Tyr	Tyr
100					95				
Glu	Leu	Lys	Thr	Gly	Gln	Gly	Phe	Thr	Tyr
110					105				

Ile Lys

- INFORMATION FOR SEQ ID NO: 90: (2)
  - SEQUENCE CHARACTERISTICS: (i)
    - (A) LENGTH: 807 bases
    - TYPE: nucleic acid (B)
    - (C) STRANDEDNESS: single

(D) TOPOLOGY	: linear
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(ii) MOLECULE TYPE: polynucleotide

# (ix) FEATURE:

(A) NAME/KEY: Nucleotide sequence encoding humanized LO-CD2a light chain variable region.

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AAGCTTCATG	ATGAGTCCTG	TCCAGTCCCT	GTTTCTGTTA	TTGCTTTGGA	TTCTGGGTAA	60
GTAGAGAATG	AGTTACAGGA	CAAGAATGGG	GATGGAGGAT	GAGTTCTGAC	TGCCCATGTT	120
GGCTGTCCAT	GTGTGGTAAG	GCAGGTCCTA	TTTTCTAAGA	TGGACACTTG	AGATTCCATT	180
ACTTGATAAT	GAGAAATTAC	AGATGAGATA	GGATTTGTGC	TAAGAGGATT	CTAATGTAGA	240
TGAGAAGGTG	TATGCCATTT	AGGATCTGCA	ACCGAATTGT	TTTGTGAAAA	AGCATTTGGT	300
ATTTTTTA	AAAATCACAA	AACACACCGG	GATCTCACAG	GAAATGAGTA	ACAAAAGTA	360
ATTCACAAAG	ATTGGTTGCA	AATTTTGCAC	ATAACTTTGT	TCTGATCTAT	TATAATTTCA	420
GGAACCAATG	GTGATGTTGT	GATGACCCAG	AGTCCACCTT	CATTATTGGT	AACCTTGGGA	480
CAACCAGCTT	CCATCTCTTG	CAGGTCAAGT	CAGAGTCTCT	TACATAGTAG	TGGAAACACC	540
TATTTAAATT	GGTTGCTACA	GAGGCCAGGC	CAATCTCCAC	AGCCGCTAAT	TTATTTGGTA	600
TCCAAACTGG	AATCTGGGGT	CCCCGACAGG	TTCAGTGGCT	CAGGGAGTGG	AACAGATTTC	660
ACACTCAAAA	TCAGTGGAGT	GGAAGCTGAG	GATGTGGGGG	TTTATTACTG	CATGCAATTT	720
ACCCATTATC	CGTACACGTT	TGGACAAGGG	ACCAAGCTGG	AAATCAAACG	TGAGTAGAAT	780
TTAAACTTTG	CTTCCTCAGT	TGGATCC				807

# (2) INFORMATION FOR SEQ ID NO: 91:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide

#### (ix) FEATURE:

(A) NAME/KEY: Humanized LO-CD2a light chain variable region.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Met Met Ser Pro Val Gln Ser Leu Phe Leu Leu

-20 -15 -10

Leu Leu Trp Ile Leu Gly Thr Asn Gly Asp

-5 -1 +1

Val Val Met Thr Gln Ser Pro Pro Ser

5 10

Leu Leu Val Thr Leu Gly Gln Pro Ala Ser

15 20

Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu

25 30

His Ser Ser Gly Asn Thr Tyr Leu Asn Trp

35 40

Leu Leu Gln Arg Pro Gly Gln Ser Pro Gln

45 50

Pro Leu Ile Tyr Leu Val Ser Lys Leu Glu

55 60

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser

65 70

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

75 80

Ser Gly Val Glu Ala Glu Asp Val Gly Val

b,

85 90

Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu

105 110

Ile Lys

#### (2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (ix) FEATURE:
  - (A) NAME/KEY: Rat LO-CD2a heavy chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu

10

Leu Gln Arg Pro Gly Ala Ser Val Lys Leu

5

15 20

Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr

25 30

Glu Tyr Tyr Met Tyr Trp Val Lys Gln Arg

35 40

Pro Lys Gln Gly Leu Glu Leu Val Gly Arg

45 50

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr

55 60

Val Glu Lys Phe Lys Lys Lys Ala Thr Leu

65 70

Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr

75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp

85 90

Thr Ala Thr Tyr Phe Cys Ala Arg Gly Lys

95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln

105 110

Gly Thr Leu Val Thr Val Ser Ser

115

## (2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide

## (ix) FEATURE:

- (A) NAME/KEY: Humanized LO-CD2a heavy chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu

5 10

Val Lys Lys Pro Gly Ala Ser Val Lys Val

15 20

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr

25 30

Glu Tyr Tyr Met Tyr Trp Val Arg Gln Ala

35 40

Pro Gly Gln Gly Leu Glu Leu Met Gly Arg

45 50

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr

55 60

Val Glu Lys Phe Lys Lys Lys Val Thr Leu

65 70

Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

75 80

Met Glu Leu Ser Ser Leu Thr Ser Asp Asp

85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys

95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln

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105 110

Gly Thr Leu Val Thr Val Ser Ser

## (2) INFORMATION FOR SEQ ID NO: 94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide

## (ix) FEATURE:

(A) NAME/KEY: Human Amu 5-3 heavy chain variable region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu

5

10

Val Lys Lys Pro Gly Ala Ser Val Lys Val

15 20

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr

25 30

Gly Tyr Tyr Met His Trp Val Arg Gln Ala

35 40

Pro Gly Gln Gly Leu Glu Trp Met Gly Arg

45 50

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Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr
				55					60

Ala Gln Lys Phe Gln Gly Arg Val Thr Met

65

70

Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
85
90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg
95 100

Thr Glu Tyr Ile Val Val Ala Glu Gly Phe
105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
115 120

Val Ser Ser

# (2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 701 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polynucleotide
- (ix) FEATURE:

( τ · )

(A) NAME/KEY: Nucleotide sequence encoding LO-CD2a heavy chain variable region.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGCTTCATG	AAATGCAGGT	GGATCATCCT	CTTCTTGATG	GCAGTAGCTA	CAGGTAAGGC	60
ACTCCCAAGT	CCTAAACTTG	AGAGATCATA	CACTTGGGAG	ACAGTGACAC	TATCTTTGGA	120
TTTCTTTCAA	CAGGGGTCAA	CTCACAGGTG	CAGCTGGTGC	AGTCTGGGGC	TGAGGTGAAG	180
AAGCCTGGGG	CCTCAGTGAA	GGTCTCCTGC	AAGGCTTCTG	GATACACCTT	CACCGAGTAC	240
TATATGTACT	GGGTGCGACA	GGCCCCTGGA	CAAGGGCTTG	AGCTGATGGG	AAGGATCGAT	300
CCTGAAGACG	GTAGTATTGA	TTATGTTGAG	AAGTTTAAGA	AAAAGGTCAC	CCTGACCGCT	360
GACACGTCCT	CTAGCACAGC	CTACATGGAG	CTGAGCAGCC	TGACCTCTGA	CGACACGGCC	420
GTGTATTACT	GTGCGAGAGG	AAAGTTTAAC	TATAGGTTTG	CTTACTGGGG	CCAAGGAACC	480
CTGGTCACCG	TCTCCTCAGG	TGAGTCCTTA	CAACCTCTCT	CTTCTATTCA	GCTTAAATAG	540
ATTTTACTGC	ATTTGTTGGG	GGGGAAATGT	GTGTATCTGA	ATTTCAGGTC	ATGAAGGACT	600
AGGGACACCT	TGGGAGTCAG	AAAGGGTCAT	TGGGAGCCCG	GGCTGATGCA	GACAGACATC	660
CTCAGCTCCC	GGACTTCATG	GCCAGAGATT	TATAGGGATC	С		701

# (2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (ix) FEATURE:

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(A) NAME/KEY: Humanized LO-CD2a heavy chain variable region.

8-1-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:
Met Lys Cys Arg Trp Ile Ile Leu Phe Leu



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-19 -15 -10

Met Ala Val Ala Thr Gly Val Asn Ser Gln

-5 -1 1

Val Gln Leu Val Gln Ser Gly Ala Glu

5

10

Val Lys Lys Pro Gly Ala Ser Val Lys Val

15 20

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr

25 30

Glu Tyr Tyr Met Tyr Trp Val Arg Gln Ala

35 40

Pro Gly Gln Gly Leu Glu Leu Met Gly Arg

45 50

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr

55 60

Val Glu Lys Phe Lys Lys Lys Val Thr Leu

65 70

Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

75 80

Met Glu Leu Ser Ser Leu Thr Ser Asp Asp

85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys

95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln

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105 110

Gly Thr Leu Val Thr Val Ser Ser 115